Amendments to the Specification:

Please replace the first full paragraph on page 25 of the specification with the following amended paragraph:

To maximize coverage of breast cancer-related genes on the microarrays used, 11,435 cDNA clones from the IMAGE consortium (Research Genetics) were obtained. These clones were selected based on literature knowledge (such as, but not limited to, preferential expression in cancer versus normal cells) and after mining (such as, but not limited to, preferential expression in breast tissues) gene expression information in the expressed sequence tags (EST) databases and the Serial Analysis of Gene Expression (SAGE) data sets available from the National Center for Biotechnology Information (NCBI, ~~http://www/ncbi.nlm.nih.gov~~ website address is www.ncbi.nlm.nih.gov).

Please replace the last paragraph on page 27 of the specification with the following amended paragraph:

Based upon the methodology of Example I above, 10 genes identified as capable of discriminating between ADH and DCIS are listed in Table 1 below along with a brief description of the gene. CloneID as used in the context of the present invention refers to the IMAGE Consortium clone ID number of each gene, the sequences of which are hereby incorporated by reference in their entireties as they are available from the Consortium at ~~http://image.llnl.gov/~~ the website "image.llnl.gov" as accessed on the filing date of the present application. Weight refers to the absolute value indicating the extent of difference in expression between ADH and DCIS where the positively signed values are expressed higher in ADH and the negatively signed values are expressed higher in DCIS; Chromosome Location refers to the human chromosome to which the gene has been assigned, and Description provides a brief identifier of what the gene encodes. The actual data corresponding to the assigned weights are shown in Figure 2.